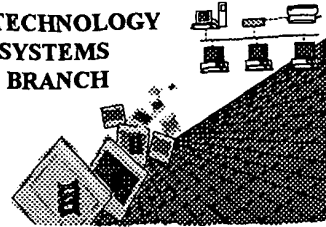


BIOTECHNOLOGY
SYSTEMS
BRANCH



1644

P#16

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/549,096B
Source: 1600
Date Processed by STIC: 9/26/2002

RECEIVED

OCT 04 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

OCT 04 2002

Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER: 09/549,096B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ✓ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

DATE: 09/26/2002

PATENT APPLICATION: US/09/549,096B

TIME: 16:28:38

Input Set : A:\LIAI-Sequence-0276397 v2.txt

Output Set: N:\CRF4\09262002\I549096B.raw

3 <110> APPLICANT: La Jolla Institute for Allergy and Immunology
 4 Ware, Carl F.
 6 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY
 7 MEDIATOR AND METHODS OF USE
 9 <130> FILE REFERENCE: 051501-0276397
 11 <140> CURRENT APPLICATION NUMBER: 09/549,096B
 12 <141> CURRENT FILING DATE: 2000-04-12
 14 <150> PRIOR APPLICATION NUMBER: 08/898,234
 15 <151> PRIOR FILING DATE: 1997-07-30
 17 <150> PRIOR APPLICATION NUMBER: 60/051,964
 18 <151> PRIOR FILING DATE: 1997-07-07
 20 <160> NUMBER OF SEQ ID NOS: 16
 22 <170> SOFTWARE: PatentIn Ver. 2.0

**Does Not Comply
Corrected Diskette Needed**

pp 1-3

ERRORED SEQUENCES

148 <210> SEQ ID NO: 6
 149 <211> LENGTH: 240
 150 <212> TYPE: PRT
 151 <213> ORGANISM: Homo sapiens
 153 <400> SEQUENCE: 6
 155 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
 156 1 5 10 15
 157 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
 E--> 158 20 20 25 25 30 30
 159 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
 E--> 160 35 35 40 40 45 45
 161 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
 E--> 162 50 55 60 65
 163 Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
 E--> 164 70 75 80
 165 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
 E--> 166 85 90 95
 167 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
 E--> 168 100 105 110
 169 Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
 E--> 170 115 120 125
 171 His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
 E--> 172 130 135 140 145
 173 Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
 E--> 174 150 155 160
 175 Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu

see p. 2, also

*misaligned
amino acid
numbers*

*see item 3
on Error
summary sheet*

RAW SEQUENCE LISTING

DATE: 09/26/2002

PATENT APPLICATION: US/09/549,096B

TIME: 16:28:38

Input Set : A:\LIAI-Sequence-0276397 v2.txt

Output Set: N:\CRF4\09262002\I549096B.raw

```

E--> 176          165          170          175
      177 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
E--> 178      180      185          190
      179 Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
E--> 180      195          200          205
      181 Leu Glu Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu
E--> 182 210          215          220          225
      183 Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
E--> 184          230          235          240
      215 <210> SEQ ID NO: 9
      216 <211> LENGTH: 21
      217 <212> TYPE: DNA
      218 <213> ORGANISM: Artificial Sequence
      220 <220> FEATURE:
      221 <223> OTHER INFORMATION: Description of Artificial Sequence:
      222 Forward primer sequence
      224 <400> SEQUENCE: 9
E--> 226 acgctgggcc tggccttctg a      21
      242 <210> SEQ ID NO: 11
      243 <211> LENGTH: 23
      244 <212> TYPE: DNA
      245 <213> ORGANISM: Artificial Sequence
      247 <220> FEATURE:
      248 <223> OTHER INFORMATION: Description of Artificial Sequence:
      249 Forward primer sequence
      251 <400> SEQUENCE: 11
E--> 253 gagctggcc tgcctgagggg cct      23
      270 <210> SEQ ID NO: 13
      271 <211> LENGTH: 22
      272 <212> TYPE: DNA
      273 <213> ORGANISM: Artificial Sequence
      275 <220> FEATURE:
      276 <223> OTHER INFORMATION: Description of Artificial Sequence:
      277 Forward primer sequence
      280 <400> SEQUENCE: 13
E--> 282 caggcdttcc tgaggggcct ca      22

```

*same error**invalid for use in the sequence itself -**Per sequence rules, use "n" and explain in <2207-<2237 section**same type of error**same*

09/549,096B 3

<400> 5

gaggttgaag gaccagggcg tgtcagccct gctccagaga ccttgggc atg gag gag 57

Met Glu Glu
1

move these under their codons

Do NOT use TAB codes; they cause misalignment
when Cbf is processed

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/549,096B

DATE: 09/26/2002
TIME: 16:28:39

Input Set : A:\LIAI-Sequence-0276397 v2.txt
Output Set: N:\CRF4\09262002\I549096B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9,11,14,20,22,24,25,26,27,29,38
Seq#:2; Line(s) 39,40,41,43,52
Seq#:3; Line(s) 53,54,55,57,66
Seq#:4; Line(s) 68,69,71,80
Seq#:5; Line(s) 81,82,85,86,139,140,141,142,143,144,145,148
Seq#:6; Line(s) 149,150,151,163,171,173,181,183,187
Seq#:7; Line(s) 189,190,192,197
Seq#:8; Line(s) 202,203,204,206,211

VERIFICATION SUMMARY

DATE: 09/26/2002

PATENT APPLICATION: US/09/549,096B

TIME: 16:28:39

Input Set : A:\LIAI-Sequence-0276397 v2.txt

Output Set: N:\CRF4\09262002\I549096B.raw

L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:158 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:226 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:253 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:282 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1